SYNOPSIS OF RESEARCH PROPOSAL

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8.	**Title of Research Project**	**:**	**EXPLORATION OF SRAP BASED GENETIC DIVERSITY FOR HYBRID DEVELOPMENT AND STABILITY ANALYSIS IN SESAME (*Sesamum indicum L.*)**

9. Introduction

India is the world's top producer of oilseed crops, which are vital to the nation's economy. After mustard and groundnuts, sesame is the third most important oilseed in India and one of the oldest crops in this group. This versatile crop, scientifically known as *Sesamum indicum* L. (family *Pedaliaceae*, 2n = 26), goes by a number of regional names, including "*Til*" in Indian homes and "Benniseed" and "Simsim" in Africa (Bhalodiya *et al.*, 2019).

Sesame is primarily a self-pollinating crop with a long history that stretches back over 5,500 years to the Indian Harappa Valley. Its seeds and oil are vital to the global food, animal feed and cosmetics industries. Its nutritional profile is equally impressive, with 15% saturated fats and 85% unsaturated fatty acids (primarily linoleic and oleic acids). It is well known that these healthy fats can reduce the risk of heart disease, cancer and damage to vital organs.

Sesame is often referred to as the "Queen of Oilseeds" due to its unique combination of antioxidants, such as sesamol, sesamin and sesamolin and its remarkable profile of unsaturated fatty acids, especially linoleic and oleic acids (Nupur *et al*., 2010). It has the highest energy density of any oilseed crop at 6,335 kcal/kg of nutritional energy (Kumar and Goel, 1994). It is a nutrient-dense powerhouse with 46–52% oil, 20–26% protein and essential amounts of calcium, phosphorus and vitamin B complex. Sesame oil is exceptionally resilient and resistant to rancidity when compared to other vegetable fats. Additionally, research has demonstrated that sesamol has potent anti-mutagenic and chemopreventive properties (Kaur and Saini, 2000; Kapadia *et al*., 2002).

Sesame is well known for its wide range of medicinal properties, which include anti-oxidative, anti-cancer, anti-hypertensive and anti-immunoregulatory properties. Sesame oil is used as a mild laxative, emollient and demulcent in pharmaceutical and medical uses; fresh leaves and seeds are traditionally used as poultices. Sesamin, a crucial bioactive substance, has shown notable hepatoprotective benefits by protecting the liver from oxidative damage. Additionally, studies by Smith and Salerno (1992) show that sesame oil can prevent human colon cancer cells from proliferating and limit the formation of malignant melanoma *in vitro*. The oil's quick skin penetration allows it to reach the bloodstream through capillaries, where it neutralizes oxygen radicals in subdermal tissues. Furthermore, by preserving high-density lipoprotein (HDL) levels while successfully lowering low-density lipoprotein (LDL) cholesterol, sesame oil consumption is associated with enhanced cardiovascular health (Sirato-Yasumoto *et al*., 2001).

The reproductive system of sesame consists of a raceme inflorescence with tubular, zygomorphic flowers that range in colour from white to purple. Eventually, these blooms grow into deeply grooved capsules that contain tiny, flat, oval seeds. Physiologically speaking, sesame is a drought-tolerant, short-day plant that thrives in temperatures between 24°C and 32°C. The typical duration of its growth cycle is 70 to 150 days. Although it is mainly used as a *Kharif* crop, it is adaptable enough for *Rabi* and summer cultivation as long as it grows in well-drained sandy loam soils and receives at least 300-400 mm of seasonal rainfall. Despite the crop's exceptional tolerance to salinity (up to 10,000 ppm) over a pH range of 5.5 to 8.2, it is nonetheless

extremely vulnerable to waterlogging and prolonged heavy rainfall, which can negatively affect its growth (Rakesh, 2022).

In India, sesame area and production were 15.53 lakh ha and 86.61 lakh tonnes, respectively, with an average productivity of 558 kg/ha (FAOSTAT, 2024). West Bengal, Madhya Pradesh, Rajasthan, Gujarat, Uttar Pradesh, Tamil Nadu, Karnataka, and Maharashtra are the main Indian states that produce sesame. Gujarat produced 1.42 lakh tonnes of sesame on 1.72 lakh hectares of land, with an average productivity of 826 kg/ha. Kachchha, Surendranagar, Junagadh, Amreli, Bhavnagar, are Gujarat's principle sesame producing districts (DoA, 2024).

India is a major producer of sesame, although its production has stalled recently and is still much lower than that of other countries that grow the crop. The economic use of heterosis presents a possible way to breach this yield plateau. In order to choose suitable parental lines and find superior cross-combinations that can produce desired transgressive segregants in the following generations, it is crucial to assess the kind and extent of heterosis. Large-scale hybrid seed production has historically been constrained by sesame autogamous (self-pollinating) nature and the absence of a consistent male sterility system, although some floral and reproductive characteristics provide a tactical advantage. In particular, the epipetalous flower form makes pollination and manual emasculation simple. Manual hybrid seed production becomes economically viable when a high seed count per capsule (40–50), a low planting rate (2.0–2.5 kg/ha) and a high seed multiplication ratio (1:250) are coupled. Seed yield and its related components has been previously reported significant heterosis in numerous studies. A cumulative or synergistic increase in the final yield can result from even slight heterotic effects in individual yield-contributing characteristics (Sasikumar and Sardana, 1990).

10. Practical Utility of the Research Project

A deeper understanding of the genetic variance among sesame genotypes is provided by the study of molecular characterization utilizing SRAP markers. It aids in the formation of divergent groups, the identification of genetically unique lines and the removal of duplicates. Such knowledge enhances the use of germplasm, encourages efficient parental selection and aids in long-term conservation initiatives. SRAP is an effective marker system technique for characterization of genetic

diversity because it has a high degree of reproducibility and discriminatory power, is simple, has a reasonable throughput rate, reveals numerous codominant markers, allows easy isolation of bands for sequencing, is more reproducible than RAPDs and easier to assay than AFLPs and most importantly, targets open reading frames (Li and Quiros, 2001).

It has been acknowledged that heterosis breeding is a useful method for giving breeders information about how to increase yield and other economic features. High productivity, consistency, enhanced quality, inherent resistance, environmental adaptability and early maturity are some examples of the hybrid vigour or superiority over parents. Nevertheless, each hybridization is never followed by the expression of hybrid vigour. Heterotic offspring are only produced by a specific pair of parents. Therefore, to estabilised an effective heterosis breeding strategies for sesame, it is necessary to clarify the genetic makeup and extent of quantitatively inherited features as well as the predicted prepotency of parents in hybrid combinations.

Yield is always considered the outcome of a many of component traits interacting with each other. Combining all of these desirable characteristics into a single variety is challenging. Therefore, in order to develop an effective breeding programme that will maximize this crops genetic enhancement, it is necessary to estimate the components of the genetic variance and understanding the type and extent of both fixable and non-fixable gene effects controlling the yield and its traits.

Diallel mating is the most common method for determining the nature and size underlying gene action within a population by measuring genetic components, GCA and SCA variances and gca and sca effects in randomly chosen parental lines. Each parent is crossed in every possible combination (except reciprocals), which is the primary benefit of a half-diallel design. Compared to full diallel design, it requires half as many matings and less experimental space for evaluation. It produces data regarding the parents and their hybrids performance.

The creation of breeding techniques to be used for crop improvement greatly benefits from an understanding of nature and the amount of gene action influencing yield and its related traits. A description of combining ability clarifies the type and extent of gene activity involved in the transmission of yield and their constituent

qualities (Sprague and Tatum, 1942). A number of biometrical methods have been developed to identify desirable parents and assess their compatibility.

Genotype × Environment interactions (G × E) result in genotypic performance (Bernardo, 2002). The G × E interaction slows down the process of selection and makes it difficult to choose high-yielding genotypes. Genotypes can be categorized according to their stable performance in various environments by evaluating the G × E interaction. They either seem to be consistent across situations or exhibit superior performance in one setting over another.

Classical models evaluate stability using high and constant mean values across environments (Lewis, 1954), whereas regression-based models use regression coefficients to select stable genotypes in different environments (Yates and Cochran, 1938; Finlay and Wilkinson, 1963). In addition to mean, Eberhart and Russell (1966) used deviation from regression as a metric to assess stability. The distinguish between environments and mega environments could not be made by any of those models.

Multivariate models such as AMMI (Gauch, 1992) and GGE biplots (Yan *et al*., 2000), have been made available to plant breeders for stability analysis and are frequently utilized in crop breeding. While, AMMI analysis is regarded as double-centered principal component analysis, GGE biplot is considered environment-centered principal component analysis. Since AMMI offers information regarding main and interaction effects in addition to a biplot and is especially useful for illustrating adaptive responses, it is typically advised as an alternative to joint regression analysis in breeding programs (Annicchiarico, 1997). To estimate G × E interaction and main effects of genotypes or environments, AMMI combines the methods of PCA (Pearson, 1901) and ANOVA (Fisher, 1918).

11. Objective

The keeping this in view, the present investigation on "**Exploration of SRAP based genetic diversity for hybrid development and stability analysis in sesame (*Sesamum indicum* L.)**" will be undertaken with the following objectives:

1. Molecular characterization of sesame genotypes using SRAP markers
2. To study the nature and magnitude of heterosis for seed yield and its component traits
3. To estimate the general ability effects of parents and specific combining ability

effects of crosses for seed yield and its component traits

4. To study the nature and magnitude of gene actions involved in the inheritance of seed yield and its component traits
5. To study the Genotype × Environment interaction and phenotypic stability using AMMI model and GGE biplot for seed yield and its component traits

12. Review of Literature

The literature pertaining to the genetic diversity, heterosis, combining ability, gene action and stability for seed yield and its component traits in sesame has been reviewed under the following subheads:

12.1 Molecular Characterization using Sequence-Related Amplified Polymorphism (SRAP)

Molecular markers play an important role in the analysis of genetic diversity and characterization of plant germplasm. PCR based marker systems such as RAPD, AFLP, RFLP, SSR, SNP and SRAP have been widely used in crop improvement studies.

Zhang *et al*. (2010) evaluated the genetic diversity of 404 native landraces from China's sesame core collection using eleven SRAP and three SSR markers. A number of 126 out of the 175 fragments that were created had an average polymorphism rate of 72%. Among the seven agro-ecological zones, Zone VII showed the greatest Nei's gene diversity (h = 0.2613) and Shannon index (I = 0.3980) values, suggesting more genetic diversity than the other zones. The genetic diversity was lowest in Zone III (h = 0.1772, I = 0.2858). The genetic links between the seven agro-ecological zones were inferred using the UPGMA method and Nei's genetic identity and genetic distance between landraces from seven zones were also investigated.

Ali AL-somain *et al*. (2017) used SRAP markers to evaluate 52 sesame accessions spanning various geographical contexts, including eight Saudi landraces for genetic diversity. Combining seventeen primers produced an abundance of alleles (365) with 100% polymorphism. The total means for primer discrimination power (DP) and polymorphism information content (PIC) were 5.88 and 0.88, respectively. With an average value of similarity 0.30 and genetic value of similarity based on Jaccard coefficients ranging from 0.12 to 0.49, the examined accessions showed both a large genetic basis and a considerable genetic remoteness. Furty-eight out of 52

accessions were sorted into seven major clusters using the unweighted pair group method with arithmetic mean (UPGMA) dendrogram, while Five accessions were kept separate because they unable to form clusters. Sub clusters, on the other hand, divided accessions and created different diversity among groups by taking into consideration the accessions geographical origin and relatedness.

Wang *et al*. (2021) assessed the genetic diversity of Jiangxi's 132 sesame germplasm samples to study using 28 SSR and 26 SRAP primers. The results showed that a total of 265 DNA bands were amplified by 28 SSR primer pairs, 221 of which were polymorphic bands, resulting in an 83.40% polymorphism ratio. Each primer pair amplified an average of 9.46 total DNA bands and 7.89 polymorphic bands. A polymorphism ratio of 44.59% was obtained by amplifying 601 DNA bands and 268 polymorphic bands using 26 different combinations of SRAP primers. 9 to 36 DNA bands and 2 to 23 polymorphic bands were amplified by each set of primers, with an average of 10.31 polymorphic bands. The genetic similarity (GS) of 132 germplasm showed a lack of overall genetic diversity, ranging from 0.5982 to 0.9607, with an average of 0.8135. The GS of six different geographic regions gradually declined from the north to the south of Jiangxi Province. Compared to northern Jiangxi, southern Jiangxi had more genetic variety in its indigenous germplasm.

Parakhia *et al*. (2025) evaluated 30 sesame accessions using SRAP markers to detect genetic diversity. Combining 109 primers gave rise to a significant number of alleles (1031) with 100% polymorphism. The total means for the SRAP primer index (SPI) and polymorphic information content (PIC) were 8.09 and 0.83, respectively. With an average score of similarity 0.40 and genetic value of similarity based on Jaccard coefficients ranging from 0.009 to 0.781, the examined accessions showed both a large genetic basis and a considerable genetic distance. Thirty accessions were sorted into two major clusters, six subclusters and four accessions using the unweighted pair group method with arithmetic mean (UPGMA) dendrogram unable to form clusters and were split separately. Conversely, sub clusters separated the accessions and produced different diversity among groups according to the accessions place of origin and relatedness. Vridhachalam JTS-8 demonstrated a broad genetic basis; unlike other accessions, it was not scattered throughout the entire dendrogram and stood out distinctly in the cluster analysis.

12.2 Heterosis

When the F_1 offspring of two genetically different parents has more or less vigor than the average of the two parents, this is called "heterosis". Shull (1914) was the first to use the term "heterosis", who also referred to this occurrence as the stimulus of heterozygosis. The superiority of a hybrid over its parents is shown by heterosis or hybrid vigour. Koelreuter (1766) was observed that as the similarity between parent's decreases, the vigour in the crosses increases. A new word called "heterobeltiosis" was proposed by Fonseca and Patterson (1968) and Mather and Jinks (1971) to explain heterozygote improvement in comparison to a better parent.

Dela and Sharma (2019) utilized 37 test entries, which comprising 28 hybrids developed through eight distinct parental lines mated in 8 × 8 diallel design without reciprocals, 8 parents and one standard check (G.Til 4). Seed yield per plant was found the most heterotic trait as it ranged from -35.63 to 31.26 % and -21.19 to 22.86 % over better parent and standard check, respectively. The crosses AT 347 × G.Til 4, AT 377 × AT 396, AT 396 × AT 404 and AT 376 × AT 377 showed high, significant and positive standard heterosis for seed yield per plant and its related traits. These crosses could be used for a useful heterosis breeding program in sesame, as these hybrids recorded 22.86, 22.77, 20.51 and 17.17 per cent higher yield, respectively, over the standard check (G.Til 4).

Nehra *et al*. (2021) crossed ten diverse parents in a half-diallel fashion to study heterosis for seed yield and its related attributes. The heterosis range observed between -25.6% (TC 25 × RT 351) and 49.53% (RT 372 × RT 103) for seed yield per plant. Out of 45 crosses, 36 exhibited positive significant heterosis and 24 positive significant heterobeltiosis for seed yield per plant. Among these crosses, cross RT 346 × TKG 22, TKG 22 × GT 10, RT 372 × GT 10, RT 372 × RT 351 and GT 10 × RT 351 were found the most promising combinations for both heterosis and heterobeltiosis with respect seed yield per plant. Out of these five crosses, only cross RT 372 × RT 351 also showed desirable heterosis/heterobeltiosis for most of associated traits *i.e*., plant height, branches per plant, capsule per plant and 100 seed weight hence that cross may be exploited in further plant breeding programme or identification of transgressive sergeants from the advanced generation.

Rathod *et al*. (2021) used a diallel mating design to study 8 parents and their fifty six F_1 hybrids. The heterosis ranged observed from -0.34 to 150.59 % mid

parent, -4.8 to 148.42 % better parent and -11.26 to 114.87 % standard heterosis. Among the 56 F_1 hybrids and reciprocals TBS 105 × R 09 (114.87%), TBS 105 × V 29 (108.97%) and TBS 7 × V 29 (106.78%) were the top promising crosses on basis of *per se* performance and standard heterosis for seed yield and its component traits. The chosen crosses for each feature have a strong potential for application in recombination breeding to produce pure lines with increased yield and oil content.

Kumar *et al*. (2022) created 21 F_1 crosses using a 7 × 7 half diallel mating to examine 14 sesame characters. The better parent heterosis ranged -35.80% to 35.23% while standard heterosis varied from -38.90% to 42.18%. The following six crosses for seed yield per plant and related component traits showed positive standard heterosis and high *per se* performance: GT 03 × SKT 1501, GT 03 × AT 307, GT 03 × AT 345, SKT 1501 × AT 307, AT 413 × AT 307 and AT 307 × AT 345. This study suggests that there is potential for both the commercialization of heterosis itself and the separation of pure lines from heterotic F_1 progenies in sesame.

Gadhiya *et al*. (2023) evaluated six parents, their 15 hybrids and standard check (G.Til 6). The hybrids were developed though half-diallel fashion. The hybrid AT 476 × Ingorala 5 reported 37.02% positive and significant heterobeltiosis for seed yield per plant followed by DC 4 × Ingorala 5 (19.19%) and AT 332 × Ingorala 5 (15.50%). The hybrids AT 476 × Ingorala 5 (48.09%), DC 4 × Ingorala 5 (28.81%) and AT 332 × Ingorala 5 (24.83%) showed significant and desirable standard heterosis.

Chaudhary *et al.* (2024) obtained twenty eight hybrids through diallel analysis utilizing eight parents. The heterobeltiosis ranged observed from -35.17% (AT 338 × JLS 2611) to 62.45% (AT 360 × ASRT 9), while range of standard heterosis was -43.15% (LT 15-28 × JLS 2611) to 30.06% (JLS 2420 × LT 15-28). The top four promising crosses on the basis of per se performance, better parent heterosis and standard heterosis for seed yield per plant were JLS 2420 × LT 15-28, AT 338 × AT 360, AT 360 × LT 15-28 and AT 360 × ASRT 9.

Kabi *et al*. (2025) evaluated 28 crosses developed by diallel mating design using eight parents for heterosis study of 14 characters. Out of the 28 crosses, 22 showed significant positive relative heterosis, 16 showed positive heterobeltiosis and just 3 showed standard heterosis for seed yield per plant. For seed yield per plant,

AT 382 with Krishna produced highest heterosis over mid-parent (92.46%), over better parent (89.32%) and over check variety (33.27 %). Krishna with Uma showed highest heterosis (58.21%) over mid-parent, over better parent (51.43%) and over standard check (47.22%) for oil content. Keeping in importance of the trait and percentage of heterosis, they identified three best cross; AT 382 with VRI 1 for early maturity, AT 382 × Krishna topped among all cross for seed yield per plant and identify Krishna × Uma as the best cross for oil percentage.

12.3 Combining ability and Gene action

The ability of a person to pass on their superior performance to their progeny is known as combining ability. It is the phenomenon that results in hybrid vigour when inbred lines are crossed. Thus, combining ability refers to a strain's capacity to generate superior offspring through hybridization with another strain.

The concept of general and specific combining ability as measure of gene action was first proposed by Sprague and Tatum (1942). This approach divides the overall genetic variance into the effects of specialized and general combining skills. While specific combining ability (SCA) is the difference between a cross combination's performance and that predicted based on the general combining ability of the parents involved in the crosses, general combining ability (GCA) is the average performance of a line in a series of crosses and is regarded as a measure of additive gene action. Specific combining ability (SCA) is regarded as an indicator of non-additive gene activity. Sca effects aid in identifying superior crossings in terms of yield and various traits, which may then be utilized in a breeding programme to take advantage of transgressive segregants.

Jeeva *et al*. (2020) conducted a diallel analysis involving five sesame genotypes to study their combining ability. A Randomized Block Design (RBD) with three replications was then used to assess 20 hybrids and their parents. The parents TMV 5 and TMV 3 and SVPR 1 considered as superior parents in relation to gca effect of seed yield per plant. Among the 20 hybrids, one hybrid VRI (SV) 2 × TMV 3 showed significant sca effect for all the traits. SVPR 1 × TMV 5 (3.83%) showed a significant and positive sca for seed yield per plant, followed by TMV3 x TMV 5 (2.47%) and TMV 6 × SVPR 1 (2.27%).

Prakash and Dasgupta (2021) conducted a 7 × 7 half dialel cross in sesame and found that GCA and SCA variations are necessary to regulate the traits. The variety Suprava and Savitri was the best general combiner for seed yield, oil content and some yield related traits. The optimum cross combinations to get desired recombinants would be Suprava × Savitri, Suprava × JLT 408 and EC 90 × Savitri for seed yield and yield related traits**.** Suprava × Savitri having additive gene control emerged as the best specific combiner for yield and its contributing traits, except oil content. Meanwhile, the hybrid IC 59 × Savitri exhibited significant positive sca effects for both seed yield and oil content, appeared to be ideal choice for getting desirable segregants.

Ramya *et al*. (2021) investigated eight sesame cultivars grown across various geographical regions of India using a full diallel cross. Hayman's analysis of six characters revealed the presence of both additive and dominance genetic variances. Over-dominance was observed in seed yield, plant height and oil content; while partial dominance was noted in capsules per plant. Regarding seed yield, parents HT 1, VRI 3 and TKG 22 were found to possess dominance genes with positive effects; similarly, Phule Til, Swetha Til and RT351 showed positive effects for capsules per plant; and crosses involving HT 1, TKG 22 and E 8 yielded segregants with high oil content. The estimation of variance components showed that both additive and dominant effects contribute to plant height and oil content, whereas additive gene effects are involved in seed yield and capsules per plant.

Sikarwar *et al*. (2021) cultivated eight parents using half-diallel design. Parents and 28 F_1 hybrids were evaluated for yield and yield-attributing traits and to determine the combining capacity. Parent TKG-22 (0.17) and JLS-120 (0.52) were the best general combiners with a significant and positive gca effect in relation to seed yield and several of its contributing traits. The following five cross combinations JTS 8 × TKG 22, JTS 8 × JLS 120, PT 2 × JLS 120, RT 366 × TKG 22 and MT 11-8-2 × RT 368 were found to be effective specific combiners for seed yield and its associated features.

Nehra *et al*. (2023) investigated the combining ability for eleven seed yield and its contributing features in 10 parents and their 45 hybrids in sesame, using a half-diallel cross. In all environmental situations, the parents RT 346, TKG 22, RT 372

and RT 351 exhibited effective general combiners for seed yield per plant and some associated features. For seed yield and oil content, the crosses RT 346 × RT 351, TKG 22 × RT 372, RT 372 × RT 351 and RT 103 × RT 351 proved to be effective specific cross combinations.

Elareny *et al*. (2025) utilized a half-diallel mating design to produce15 F_1 crosses from six genetically distinct parental lines. These parental lines and hybrids were evaluated in a Randomized Block Design (RBD) with three replications. The Baker ratio varied from moderate to high for most traits, indicating the prevalence of additive gene action. However, non-additive effects were also observed in few traits. Among the three crosses, $P_1 \times P_5$, $P_2 \times P_3$ and $P_3 \times P_6$, favourable combinations were identified for early flowering, height of plant and length of capsule traits that are conducive to increasing seed yield. Specifically, $P_1 \times P_5$, $P_2 \times P_3$ and $P_3 \times P_6$ excelled in early flowering and height of plant, while $P_4 \times P_5$ demonstrated superiority in relation to branching, seed weight and oil content.

Mungala *et al*. (2025) developed 45 hybrids from a half-diallel cross involving ten genotypes of sesame. Low estimates of the potence ratio indicated that, with the exception of oil content, non-additive gene action predominated in all other traits. The estimation of gca effects the parental line Keriya 10, U 6-3 and ST 12-25 demonstrated good general combiners for seed yield per plant. The crosses Keriya 10 × BS 6-1, U 6-3 × Khadkala 1 and U 6-3 × EI 233 were identified as excellent specific combiners for seed yield per plant and its associated traits. Crosses exhibiting high SCA effects for seed yield per plant were observed to involve parents characterized as good × poor general combiners.

12.4 Genotype × Environment Interaction (GEI) and stability analysis

An individual phenotypic expression is influenced by their genotype, environment and G × E interaction. G × E interactions are particularly important because they exhibit different relative genotype performance that alter the genotype ranking in diverse environments (Fernandez, 1991). G × E interactions can be classified as either qualitative or quantitative depending on how they affect the environment (Peto, 1982). Selecting and identifying the best-performing genotypes in distant environments is made more difficult by the qualitative kind of G × E interactions. Both parametric and non-parametric methods were proposed by

Romagosa and Fox (1993) and Huehn (1990) to investigate the G × E interactions and adaptation.

The genotype stability is only determined for a few extreme environments when only few low and high yielding conditions are used for the analysis. Second, the assumption that interaction and environmental means have a linear association is actually multivariate and errors associated with genotype slopes are not statistically independent (Crossa *et al*., 1990).

The principal components analysis provided by Pearson (1901) is the basis for the Genotype + Genotype × Environment interaction (GGE) and additive main effect and multiplicative interactions (AMMI) biplot models, which are linear-bilinear models with an additive component (the main effect of the environment or genotypes) and a multiplicative component (the G × E interaction). In GGE biplot, the graphical representation is done without separating the additive and multiplicative components (Yan *et al*., 2010), but in AMMI, the components are divided during stability analysis without confounding factors (Gauch *et al*., 2008) and then combined during biplot preparation (Gabriel, 1971). According to several studies (Zobel *et al*., 1988; Yan *et al*., 2000; Ebdon and Gauch, 2002; Samonte *et al*., 2005), these models are strong instruments for the efficient analysis and interpretation of multi-environment data structures in breeding programmes.

Gauch (1988) developed a stability analysis based on the AMMI model, which combines two statistical methods: principal component analysis (Pearson, 1901) and analysis of variance (Fisher, 1918). After comparing the models of AMMI, GGE and singular value decomposition based statistical analysis, he concluded that independent impacts of G, E and GEI should be used for agricultural trial analysis. The AMMI model can address the various opportunities and problems presented by the distinct effects of G, E and GEI.

Sirisha *et al*. (2022) investigated eight sesame cultivars during the *Kharif* 2017, 2018 and 2019. Environment A (*Kharif* 2017) had higher mean values of 650 kg/ha for seed yield, while Environment B (*Kharif* 2018) had higher mean values of 49% for oil percentage. The genotypes 4 (YLM 142) (696.97 kg/ha) and 6 (YLM 146) (734.15 kg/ha) had higher mean values for seed yield than the grand mean with stronger G × E interaction effects, demonstrating excellent performance in favourable

conditions. Despite having a lower yield (564.54 kg/ha) than YLM 142 and YLM 146, genotype 8 (YLM 66) was found to have a nearly zero interaction principal component analysis (IPCA) score and a sustained yield across environments. The oil percentage (47.78%) of genotype 8 (YLM 66) was higher than the grand mean (46.85%) and it was shown to be stable and more adaptable across three environments when it was close to the IPCA zero axis. The genotype 6 (YLM 146) performed well in favourable or particular conditions, as seen by its higher mean value (48.57%) compared to the grand mean and greater G × E interaction effects for oil percentage.

Azon *et al*. (2023) used 19 sesame accessions in eight different conditions. During the 2020 growing season, the accessions were assessed for three characteristics: seed yield, 1000 seed weight and days to 50% flowering. G10 and G13 were found to be high seed producing accessions that were suited to environments E_1 and E_2. The best accessions for seed yield were G11 and G13 in the first, G10 in the second and G3 and G8 in the third mega-environment. G10, G5 and G12 were found to be high seed producing and environmentally stable accessions by AMMI and GGE studies. Based on their representativeness and discriminating power, GGE biplot showed that E_1 and E_2 were the best settings for multi-location trials. G10, G13 and G19 were identified by Multi Threat Stability Index (MTSI) as promising germplasm that should be suggested for a breeding effort.

Shaibu *et al*. (2025) assessed 15 genotypes in four locations in order to find stable and high yielding sesame genotypes. The maximum grain yield was 447.76 kg/ha for NCRIBEN02M and 424.08 kg/ha for NCRIBEN04E. Environment, genotype and GEI all had significant ($p < 0.01$) effects on sesame yield, according to the AMMI ANOVA. NCRIBEN02M was shown to be the most stable genotype by parametric and AMMI studies, whereas Kangarawa was ranked as the best by the MTSI, which takes into account several characteristics. The study suggests Kangarawa for multi-trait stability and NCRIBEN02M for its high yield and wide stability.

Takele and Dhabessa (2025) studied 16 genotypes of sesame that were grown in six different environments using a randomized full block method. The first four interaction principal axes (IPCA1, IPCA2, IPCA3, and IPCA4) were found to be highly significant ($p < 0.001$) with contributions of 43.55%, 30.60%, 20.66% and

2.94% of the total Genotype × Environment interaction, respectively. G03 (43.55%) and G10 (20.84%), which had the highest yield, were positioned on a GGE biplot with a near-concentric circle and was more stable than other tested genotypes. As a result, these two genotypes were chosen as viable options for sesame genotypes that might be introduced into the ecosystems under test.

Takele *et al*. (2026) evaluated 16 sesame genotypes under six different conditions. GGE biplots and the AMMI model were used to estimate stability analysis. Highly significant ($p < 0.01$) differences across environments, genotypes, GE interaction and four IPCAs were found using AMMI analysis of variance. The first four IPCAs (IPCA1, IPCA2, IPCA3, and IPCA4) showed high significance and contributed 56.3%, 23.9%, 11.3%, and 2.3% of the total GE interaction, respectively. Genotypes G15 and G4 had higher with close to concentric circles indicating the wide adaptability over the tested environments and similar agroecology.

13. Materials and Methods

Genetic diversity analysis of 60 genotypes will be carried out using Sequence-Related Amplified Polymorphism (SRAP) markers. Out of these 60 genotypes 10 will be selected on the base of diversity present in the genotypes. The selected 10 genotypes will be crossed in diallel fashion excluding reciprocals to produce 45 F_1 hybrids. The experimental material will be comprised of 56 entries including 45 F_1 hybrids, 10 parental genotypes and one standard check G.Til 21. The evaluation will be carried out at four different locations, *i.e*., Junagadh, Amreli, Kodinar and Jam Khambhalia.

13.1 Location

(a) For genetic diversity analysis using SRAP

Department of Genetics and Plant Breeding, JAU, Junagadh.

(b) For hybridization

Instructional Farm, College of Agriculture, JAU, Junagadh.

(c) For evaluation

1. Instructional Farm, College of Agriculture, JAU, Junagadh.
2. Agricultural Research Station, Amreli
3. Dry Farming Research Station, Jam Khambhalia

4. Main Sugarcane Research Station, Kodinar

13.2 Year and season of experiment

(a) Genetic diversity analysis using SRAP

(b) Development of crosses during *Kharif* 2026

(c) Evaluation of experimental material in four different locations during summer 2027

13.3 Treatment details: 56 entries **(**45 hybrids + 10 parents + 1 check)

Sixty genotypes will be subjected to molecular characterization using SRAP markers and ten diverse parents will be selected based on genetic diversity. These selected parents will be crossed in a half-diallel mating design during *Kharif* 2026 to produce 45 F_1 hybrids. The variety G.Til 21 will be used as a standard check for estimating standard heterosis.

List of genotypes for molecular characterization using SRAP

Sr. No.	Genotype	Sr. No.	Genotype
1	Keriya 5	31	SPS 34
2	NIC 9464	32	IS 312
3	IC 199433	33	SG 826
4	IC 20528	34	Khad Kala 2
5	NIC 8476	35	Zira 3
6	KMR 69	36	AT 607
7	NIC 8526	37	AT 374
8	IC 43063	38	AT 603
9	IC 127278	39	AT 565
10	BS 6-1-1	40	AT 542
11	ES 347	41	AT 569
12	DC 29-5	42	AT 518
13	HT 15	43	SKT 2308
14	DC 10-43	44	SKT 2304
15	ES 22	45	SKT 2314
16	IS 222	46	SKT 2306
17	U 62-11	47	SKT 2406

18	DC 28	48	SKT 2403
19	IS 209	49	G.Til 1
20	Keriya Chard 1	50	G.Til 2
21	U 1	51	G.Til 3
22	Anand 13	52	G.Til 4
23	Charodiya 1	53	GJT 5
24	ST 768	54	G.Til 6
25	IS 51	55	G.Til 7
26	ES 631	56	G.Til 8
27	Anand 64	57	G.Til 9
28	JLT 3	58	G.Til 10
29	MT 62-18	59	G.Til 11
30	SPS 27	60	G.Til 21

13.4 Experimental design **:** Randomized Block Design

13.5 Number of replications **:** Three

13.6 Spacing **:** 30 × 10 cm

13.7 Observations to be recorded

Five randomly selected competitive plants from each entry, excluding border plants, will be chosen to record observations on various traits and the average will be used for statistical analysis. Days to 50% flowering and days to maturity will be recorded on plot basis. The detailed procedure adopted for recording various observations will be as under:

13.7.1 Days to 50 per cent flowering

The number of days counted from the date of sowing to the emergence of flowers in approximately 50% of the plants in a plot will be considered as days to 50% flowering.

13.7.2 Days to maturity

The number of days taken from sowing to physiological maturity on plot basis will be considered as days to maturity.

13.7.3 Plant height (cm)

The height of plant will be measured in centimeters from ground level to the tip of main shoot at the time of maturity.

13.7.4 Number of branches per plant

The total number of branches arising directly from the main stem will be counted at the time of maturity.

13.7.5 Length of capsule (cm)

Length from the base to the tip of capsule will be recorded in centimeters from each selected plants for five capsules per plant and then average value will be computed.

13.7.6 Number of capsules per plant

Total number of capsules of selected plants will be counted and recorded at the time of maturity.

13.7.7 Number of seeds per capsule

The seeds from five capsules of each selected plants will be counted manually and the average value will be worked out.

13.7.8 1000 seed weight (g)

This will be recorded by taking random sample of the well mixed bulk product from each genotype. One thousand seeds will be counted manually, weighted in grams on an electronic balance and the average value will be worked out.

13.7.9 Seed yield per plant (g)

Seeds harvested from selected plants will be dried, cleaned and weighted in grams on an electronic balance and average value will be computed.

13.7.10 Biological yield per plant (g)

After harvesting and drying of plants, total dry weight of plant will be recorded individually in grams.

13.7.11 Harvest index (%)

It will be calculated in percentage by using following formula:

$$\text{Harvest index (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100\%$$

13.7.12 Oil content (%)

Seed samples will be drawn randomly from the bulk product on plot basis and oil content will be determined by using Nuclear Magnetic Resonance (NMR analyzer) as suggested by Tiwari *et al.* (1974).

14. Statistical Analysis

For each character, the mean values of the parents, F_1 hybrids and check will be statistically analyzed in the following ways:

14.1 Molecular characterization using SRAP markers

DNA extraction and purification based on Cetyl Trimethyl Ammonium Bromide (CTAB) method with modification if required will be used as described by Doyle and Doyle (1990). Good quality DNA will be used for PCR amplification of molecular markers. PCR amplification and gel electrophoresis will be carried out by using SRAP (Sequence Related Amplified Polymorphism) markers. The PCR amplified DNA bands will be scored and marker analysis will be carried out using suitable software.

The observation on molecular marker will be recorded individually for each marker and summary statistics of the molecular marker data will be estimated using suitable software. The dendrogram will be generated using appropriate software.

14.1.1 DNA isolation

DNA samples will be extracted using Cetyl Trimethyl Ammonium Bromide (CTAB) method of DNA extraction given by Doyle and Doyle (1990). Good quality DNA will be used for PCR amplification of molecular markers.

14.1.2 PCR amplification

The primers will be retrieved from the available literature. PCR amplification will be carried out in 10 ul of reaction containing 10 picomole of primer and 100 ng/ul of DNA template.

14.1.3 Gel electrophoresis

The PCR amplified products will be resolved on 3.0 per cent agarose gel in 1X TBE buffer and will be visualized under UV using gel documentation system.

14.1.4 Scoring of data

The PCR amplified DNA bands will be scored as per the dominant nature of SRAP marker.

14.1.5 Marker analysis

The scored bands or alleles will be subjected to suitable molecular data analysis software.

14.2 Analysis of variance for experimental design

The analysis of variance for the experimental design will be carried out using Randomized Block Design separately for all the characters as per Panse and Sukhatme (1995).

14.3 Estimation of heterosis

While estimating heterosis, heterobeltiosis will be evaluated using data from the better parent to assess the superiority of the hybrid. Similarly, standard heterosis, also known as economic heterosis, will be determined by comparing the hybrid with a suitable check variety (G.Til 21) to evaluate its practical performance.

(A) Heterobeltiosis

According to Fonseca and Patterson (1968), heterobeltiosis is determined as the deviation of F_1 above the better parent. The method to represent this deviation in percentage is as follows:

$$\text{Heterobeltiosis (\%)} = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where,

$\bar{F}_1$ = Mean performance of F_1

$\overline{BP}$ = Mean value of better parent of respective cross combination

(B) Standard heterosis

It is superiority of F_1 over the standard commercial variety (G.Til 21) and will be calculated as below:

$$\text{Standard heterosis (\%)} = \frac{\overline{F}_1 - \overline{SC}}{\overline{SC}} \times 100$$

Where,

$\overline{F}_1$ = Mean performance of F_1

$\overline{SC}$ = Mean performance of the standard check commercial variety (G.Til 21)

14.4 Analysis of variance for combining ability and gene action

The Griffing (1956) recommended half-diallel mating design will be used to perform the combining ability analysis.

14.5 Components of Genetic Variance

Numerical approach of Hayman (1954) will be used to work out components of genetic variation and other genetic ratios.

14.6 Analysis of variance for G × E interactions

The statistical analysis for Genotype × Environment interaction and phenotypic stability will be carried out according to AMMI model for seed yield and its components.

14.7 GGE biplot

GGE biplot analysis will be carried out to evaluate the performance of genotype and stability across different environments. The method described by Yan and Kang (2003) will be used to graphically present the genotype main effect (G) and Genotype × Environment interaction (GE).

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